Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

CLAIMS

1-39 (Canceled)

40. (Canceled)

70 (New) A method of preparing DNA fragments from a sample of nucleic acids to be analyzed, which method comprises selectively fragmenting the nucleic acids, comprising the steps of:

a) preparing first double-stranded DNA fragments F1 using at least one type II restriction enzyme E1 which randomly fragments the sample of nucleic acids to be analyzed, and generating said DNA fragments F1 with blunt or cohesive ends;

b) obtaining DNA fragments F'1 by ligating the 5'-end of said DNA fragments F1 obtained in step a) to a first double-stranded adapter AA' so as to form a junction sequence located at the junction of the 3'-end of said first double-stranded adapter AA' and the 5'-end of said DNA fragments F1, wherein said junction sequence consists of the 5'-terminal one or more base pairs but not the entire sequence of the recognition site of a type of IIS restriction enzyme E2, the cleavage site of which is located downstream of said recognition site, and wherein said junction sequence contains at its 3'-end the 3'-terminal one or more base pairs of the E1 restriction enzyme restriction site;

c) obtaining a fraction of short DNA fragments F2 through selective cleavage by said restriction enzyme E2, of a fraction of the DNA fragments F'1 obtained in step b) which are formed of said first double-stranded AA' and the DNA fragments F1 generated in step a) whose sequence contains at its 5'-end, the sequence of the 3'-terminal one or more base pairs of the recognition site of said restriction enzyme E2, which 3'-terminal base pairs together with the 5'-terminal base pairs from said junction sequence can form the entire recognition site of the restriction enzyme E2; and

d) purifying said fraction of short DNA fragments F2.

41. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein step a) is carried out with two different E1 restriction enzymes, E1e and E1c, such that:

at least one generates cohesive ends, different from those optionally generated by the other restriction enzyme, and

the 3' end of $E1_A$ restriction site is that of the unit as defined in step b).

42. (Previously Presented) The method as claimed in claim 41, wherein one of the enzymes cleaves frequently and the other rarely.

43. (Previously Presented) The method as claimed in claim 42, wherein: the enzyme that cleaves frequently is the enzyme $E1_A$, which enzyme $E1_A$ generates at least one end of a fragment F1 that binds to the adapter AA' in step b), and the enzyme that cleaves rarely, is the enzyme $E1_C$ which generates at least one end of a fragment F1, which binds, in step b), to a second adapter CC' that is different from the adapter AA'.

44. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein steps a) and b) are carried out simultaneously.

45. (Currently Amended) The method as claimed in claim ~~40~~ 70, which further comprises purifying the fragments less than 1000 bp, prior to the ligation step b).

46. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein the adapter AA' as defined in step b) comprises, at the 3' end of the strand A or 5' end of the strand A', or both, a zone 1 of approximately 1 to 8 bases or base pairs, which is partially or completely identical or complementary to the restriction site of the enzyme E1, which zone 1 is chosen so as to reconstitute the sequence of the first N-x bases or base pairs of the recognition site of the restriction enzyme E2, by ligation of said adapter AA' to the ends of said DNA fragments obtained in a).

47. (Previously Presented) The method as claimed in claim 46, wherein zone 1 includes one or more mismatches with the sequence of said cleavage site of the restriction enzyme E1.

48. (Previously Presented) The method as claimed in claim 46, wherein the adapter as defined in step b) comprises, upstream of the zone 1, a zone 2 of at least 6 base pairs.

49. (Previously Presented) The method as claimed in claim 48, wherein the adapter as defined in step b) comprises at least one base located between the zone 1 and the zone 2, different from that which, in the cleavage site of the restriction enzyme E1, is immediately adjacent to the complementary sequence corresponding to the zone 1.

50. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein the adapter as defined in step b) comprises a phosphate residue covalently linked to the 5' end of the strand A'.

51. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein, when said method consists of a single selection of short fragments according to steps a) to d), it comprises at least one additional step b'), c') or d') or a combination thereof comprising amplifying the fragments F'1 or F2 using a pair of primers.

52. (Currently Amended) The method as claimed in claim ~~40~~ 70, wherein the adapter AA' as defined in step b) is linked, at the 5'end of its strand A, to a label.

53. (Previously Presented) The method as claimed in claim 43, wherein the 5' end of the strand C' of the adapter CC' is linked to a label, which label is attachable to a functionalized solid support.

54. (Previously Presented) The method as claimed in claim 53, wherein the fragments F'1 obtained in step b) or b') are brought into contact with said functionalized support prior to the cleavage step c), and the fraction of short fragments F2 of step d) corresponds to the fraction of fragments that is either retained on said support (adapter AA' linked to the label that attaches to the support) or free (adapter CC' linked to the label that attaches to the support).

55. (Currently Amended) The method as claimed in claim ~~40~~ 70, which comprises an additional step d') or g) comprising obtaining single-stranded fragments from the short fragments F2 obtained in step d) or d') or else from the short fragments F'2 obtained in step f).

56. (Previously Presented) The method as claimed in claim 1, which further comprises purifying the amplification products obtained in step b'), c'), d') or f) or of the single-stranded fragments obtained in step d') or g).

57. (Currently Amended) A short DNA fragment, representing a genetic marker, obtained by the method as claimed in claim ~~40~~ 70, which has a sequence of less than 100 bases or base pairs, comprising at least one specific sequence consisting of a fragment of genomic sequence or of cDNA sequence bordered, respectively, by the recognition site and the cleavage site of a restriction enzyme E2, the cleavage site of which is located downstream of said recognition site, such that the 5' end of said specific sequence corresponds to the last x base pairs of the recognition site - having N base pairs - of said enzyme E2, with $1 \leq x \leq N-1$, said marker including, at each end, at least 6 bases or 6 base pairs of nonspecific sequence.

58. (Previously Presented) The DNA fragment as claimed in claim 57, which is a single-stranded fragment.

59. (Previously Presented) The DNA fragment as claimed in claim 57, which is linked, at one of its 5' ends, to an appropriate label.

60. (Previously Presented) The method as claimed in claim 51, wherein the pair of primers are a pair of labeled primers.

61. (Previously Presented) The method as claimed in claim 52, wherein the label is a label for detecting nucleic acid hybrids.

62. (Previously Presented) The method as claimed in claim 52, wherein the label is attachable to a functionalized solid support.

63. (Previously Presented) The method as claimed in claim 52, wherein the label which is linked to the first double-stranded adapter AA' is attachable to a functionalized support, and wherein the DNA fragments F'1 obtained in step b) are brought into contact with said functionalized support prior to the cleavage step c), and the fraction of

short fragments F2 of step d) corresponds to the fraction of fragments that is retained on said support.

64. (Currently Amended) The method as claimed in claim ~~40~~ 70, which further comprises a second collection of one or more subset(s) of fragments from the fraction of short DNA fragments F2 obtained in step d) following the steps of:

e) ligating the end of the short DNA fragments F2 obtained in d) which is not linked to the first double-stranded adapter AA' to at least a third complementary double-stranded adapter BB', thereby producing short fragments F'2; and

f) amplifying the short DNA fragments F'2 linked to said double-stranded-adapters, using at least one pair of primers, so as to select at least one subset of short DNA fragments F'2 from the fraction of short fragments F2 obtained in d).

65. (Previously Presented) The method as claimed in claim 64, wherein one of the primers of step f) is labeled at its 5' end.

66. (Previously Presented) The method as claimed in claim 64, wherein step e) comprises ligating several different complementary double-stranded adapters BB', each comprising a specific sequence of 1 to 10 bases, at the 5' end of the strand or at the 3' end of the strand B.

67. (Previously Presented) The method as claimed in claim 64, wherein said double-stranded adapter BB' of step e) comprises a phosphate residue covalently linked to the 5' end of the strand B.

68. (Previously Presented) The method as claimed in claim 64, which further comprises obtaining single-stranded fragments from the short DNA fragments F'2.

69. (Previously Presented) The method as claimed in claim 64, which further comprises purifying the amplification products of said short DNA fragments F'2.